

(D) TOPOLOGY: linear  
- (ii) MOLECULE TYPE: DNA  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:  
# 12

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## CLAIMS:

We claim:

1. A method for inhibiting telomerase activity in human cells, comprising contacting the cells with a polynucleotide comprising a nucleotide sequence of at least 25 consecutive nucleotides which is substantially identical or substantially complementary to a human telomerase RNA component sequence, wherein the polynucleotide inhibits endogenous telomerase activity.
2. The method of claim 1, wherein the cells are cancer cells.
3. The method of claim 1 wherein the nucleotide sequence is identical to a human telomerase RNA component sequence.
4. The method of claim 1 wherein the nucleotide sequence is complementary to a human telomerase RNA component sequence.
5. The method of claim 1 wherein the nucleotide sequence is a mutated sense sequence of human telomerase RNA component.
6. The method of claim 1 wherein the polynucleotide is a ribonucleic acid or a deoxyribonucleic acid.
7. The method of claim 1 wherein the polynucleotide is between 25 and 50 nucleotides long.
8. The method of claim 1 wherein the polynucleotide is between 25 and 200 nucleotides long.
9. The method of claim 1 wherein the nucleotide sequence is selected from a contiguous sequence contained within a human genomic DNA sequence encoding the RNA component of human telomerase located in an .about.2.5 kb HindIII-SacI insert of plasmid pGRN33 (ATCC 75926).
10. The method of claim 1 comprising transfecting the cell with an expression vector comprising a heterologous transcription regulatory sequence operably linked to a nucleotide sequence that encodes the polynucleotide, wherein the transcription regulatory sequence promotes transcription of the polynucleotide in the cell.
11. The method of claim 10, wherein the heterologous transcriptional regulatory sequence comprises a promoter which is constitutively active in human cells.
12. The method of claim 10, wherein said expression vector produces antisense RNA complementary to human telomerase RNA component.
13. The method of claim 10 wherein the nucleotide sequence of at least 25 consecutive nucleotides is complementary to a sequence of human telomerase RNA component.
14. The method of claim 10 wherein the expression vector is an adenovirus-based vector.
15. The method of claim 10 wherein the heterologous transcriptional regulatory sequence is selected from metallothionein promoter, constitutive adenovirus major late promoter, dexamethasone-inducible MMTV promoter, SV40 promoter, MRP polIII promoter, constitutive MPSV promoter, tetracycline-inducible CMV

promoter, and constitutive CMV promoter.

16. The method of claim 1 wherein the polynucleotide is a synthetic polynucleotide.

17. The method of claim 16 wherein the polynucleotide comprises one or more non-naturally occurring nucleotides or nucleotide linkages.

18. The method of claim 16 wherein the polynucleotide comprises a moiety selected from the group consisting of a methylphosphonate moiety, a C-5 propynyl moiety, and a 2'-fluororibose sugar moiety or is selected from the group consisting of a phosphorothioate polynucleotide, an O-methyl polynucleotide, a polyamide polynucleotide, and a PNA polynucleotide.

19. The method of claim 16 wherein the polynucleotide comprises a nucleotide sequence selected from:

5'- CUCAGUUAGG GUUAGACAAA -3' (SEQ ID NO:41);

5'- CGCCCUUCUC AGUUAGGGUU AG -3' (SEQ ID NO:42);

5'- GGCGCCUACG CCCUUCUCAG UU -3' (SEQ ID NO:43); or

5'- CAGGCCCAACC CTCCGCAACC -3' (SEQ ID NO:8).

20. A method for inhibiting telomerase activity in human cells, comprising contacting the cells with a polynucleotide comprising a nucleotide sequence of at least 10 consecutive nucleotides which is identical or complementary to a human telomerase RNA component sequence, wherein the polynucleotide does not comprise the sequence TTAGGGTTAGGG (SEQ ID NO:44) and wherein the polynucleotide inhibits endogenous telomerase activity.

21. The method of claim 20 wherein the cells are cancer cells.

22. The method of claim 20 wherein the nucleotide sequence is identical to a human telomerase RNA component sequence.

23. The method of claim 20 wherein the nucleotide sequence is complementary to a human telomerase RNA component sequence.

24. The method of claim 20 wherein the polynucleotide is a ribonucleic acid or a deoxyribonucleic acid.

25. The method of claim 20 wherein the nucleotide sequence encoding the polynucleotide is selected from a contiguous sequence contained within a human genomic DNA sequence encoding the RNA component of human telomerase located in an about 2.5 kb HindIII-SacI insert of plasmid pGRN33 (ATCC 75926).

26. The method of claim 20 wherein the polynucleotide is a synthetic polynucleotide.

27. The method of claim 26 wherein the polynucleotide comprises one or more non-naturally occurring nucleotides or nucleotide linkages.

28. The method of claim 26 wherein the polynucleotide comprises a moiety selected from the group consisting of a methylphosphonate moiety, a C-5 propynyl moiety, and a 2'-fluororibose sugar moiety or is selected from the group consisting of a phosphorothioate polynucleotide, an O-methyl polynucleotide, a polyamide polynucleotide, and a PNA polynucleotide.

29. The method of claim 20 comprising transfecting the cells with an expression vector comprising a heterologous transcription regulatory sequence operably linked to a nucleotide sequence encoding the polynucleotide, wherein the transcription regulatory sequence promotes transcription of the polynucleotide in the cell.

30. The method of claim 29 wherein the heterologous transcriptional regulatory sequence comprises a promoter which is constitutively active in human cells.

31. The method of claim 29 wherein the nucleotide sequence of at least 10 consecutive nucleotides is complementary to a sequence of human telomerase RNA component.

32. The method of claim 29 wherein the expression vector is an adenovirus-based vector.

33. The method of claim 29 wherein the heterologous transcriptional regulatory sequence is selected from the group consisting of metallothionein promoter, constitutive adenovirus major late promoter, dexamethasone-inducible MMTV promoter, SV40 promoter, MRP polIII promoter, constitutive MPSV promoter, tetracycline-inducible CMV promoter, and constitutive CMV promoter.

5' end, followed by a sequence that is specific for the target (see FIG. 3, primer 1), in combination with appropriate return primer (primer 2), and a third primer that consists solely of the repetitive sequence (primer 3, e.g. [5'-TTTCCC-3']<sub>4</sub>) (SEQ ID NO:40) to amplify the specific target in in situ PCR. The presence of the primer 3 will elongate the PCR product due to the staggered-binding of the primer 3 to 3'-end of the target PCR product. The elongation of the PCR products can be induced by decreasing the annealing temperature of the initial PCR condition.

- 163 For example, if the annealing temperature of the target sequence in the primer 1 is 60.degree. C., the sample will be initially amplified for 15-20 cycles of 94.degree. C./45.degree. C. and 60.degree. C./45.degree. C., then it will be amplified for 15-20 cycles of 94.degree. C./45.degree. C. and 50.degree. C./45.degree. C. Lowered annealing temperature in the second PCR step will favor the generation of the elongated PCR products by increasing the chance of stagger-binding of primer 3 to the repetitive sequences. The resulting elongated PCR products will be less prone to leakage through the cellular matrix, thus resulting in a better signal retention in in situ PCR analysis.
- 164 The foregoing examples describe various aspects of the invention and how certain nucleic acids of the invention were made. The examples are not intended to provide an exhaustive description of the many different embodiments of the invention encompassed by the following claims.

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# SEQUENCE LISTING

- (1) GENERAL INFORMATION:

- (iii) NUMBER OF SEQUENCES: 44

- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 18 base

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

# 18 GG

- (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 560 base

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: RNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

- GGGUUGCGGA GGGUGGGCCU GGGAGGGGUG GUGGCCAUUU UUUGUCUAAAC CC - #UACUGAG  
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- AAGGGCGUAG GCGCCGUGCU UUUGCUCUCCC GCGCGCUGUU UUUCUCGCUG AC - #UUUCAGCG  
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- GGCAGAAAAG CCUCGGCCUG CCGCCUCCA CCGUUCAUUC UAGAGCAAAC AA - #AAAAUGUC  
180

- AGCUGCUGGC CCGUUCGCCC CUCCCGGGGA CCUGCGGCGG GUCGCCUGCC CA - #GCCCCCGA  
240

- ACCCCGCCUG GAGGCCGCGG UCGGCCCGGG GCUUCUCCGG AGGCACCCAC UG - #CCACCGCG  
300

- AAGAGUUGGG CUCUGUCAGC CGCGGGUCUC UCGGGGGCGA GGGCAGGUU CA - #GGCCUUUC  
360

- AGGCCGCGAGG AAGAGGAACG GAGCGAGUCC CCGCGCGCGG CGCGAUUCCC UG - #AGCUGUGG  
420

- GACGUGCACC CAGGACUCGG CUCACACAUG CAGUUCGCUU UCCUGUUGGU GG - #GGGGAACG  
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- CCGAUCGUGC GCAUCCGUCA CCCUCGCCG GCAGUGGGGG CUUGUGAACC CC - #CAAACCG  
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              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: RNA
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              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: DNA (genomic)
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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  60
- AGCAATAGGA ATTTAAAAAA AGAAATTATG AAAACTGACA AGATTTAGTG CC - #TACTTAGA
  120
- TATGAAGGGG AAAGAAGGGT TTGAGATAAT GTGGGATGCT AAGAGAATGG TG - #GTAGTGTT
  180
- GACATATAAC TCAAAGCATT TAGCATCTAC TCTATGTAAG GTACTGTGCT AA - #GTGCAATA
  240
- GTGCTAAAAA CAGGAGTCAG ATTCTGTCCG TAAAAAACTT TACAACCTGG CA - #GATGCTAT
  300
- GAAAGAAAAA GGGGATGGGA GAGAGAGAAG GAGGGAGAGA GATGGAGAGG GA - #GATATTTT
  360
- ACTTTTCTTT CAGATCGAGG ACCGACAGCG ACAACTCCAC GGAGTTTATC TA - #ACTGAATA
  420
- CGAGTAAAAC TTTTAAGATC ATCCTGTCAT TTATATGTAA AACTGCACTA TA - #CTGGCCAT
  480
- TATAAAAATT CGCGGCCGGG TGCGGTGGCT CATACCTGTA ATCCCAGCAC TT - #TGGGAGGC
  540
- CGAAGCGGGT GGATCACTTG AGCCCTGGCG TTCGAGACCA GCC'TGGGCAA CA - #TGGTGAAA
  600
- CCCCCGTCTC TACTAAAAAC ACAAAAAC TA GCTGGGCGTG GTGGCAGGCG CC - #TGTAATCC
  660
- CAGCTACTCA GGAGGCTGAG ACACGAGAAT CGCTTGAACC CGGGAGCAGA GG - #TTGCAGTG
  720
- AGCCGAGATC ACGCCACTAG ACTCCATCCA GCCTGGGCGA AAGAGCAAGA CT - #CCGTCTCA
  780
- AAAAAAAAAA TCGTTACAAT TTATGGTGGA TTA TCTCCCTT CTTTTTACCT CA - #TCAAGACA
  840
- CAGCACTACT TTAAAGCAAA GTCAATGATT GAAACGCCTT TCTTTCCTAA TA - #AAAGGGAG
  900
- ATTCAGTCCT TAAGATTAAT AATGTAGTAG TTACACTTGA TTAAAGCCAT CC - #TCTGCTCA
  960
- AGGAGAGGCT GGAGAAGGCA TTCTAAGGAG AAGGGGGCAG GGTAGGA ACT CG - #GACGCATC
  1020
- CCACTGAGCC GAGACAAGAT TCTGCTGTAG TCAGTGCTGC CTGGGAATCT AT - #TTTCACAA
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- AGTTCTCCAA AAAATGTGAT GATCAAAACT AGGAATTAGT GTTCTGTGTC TT - #AGGCCCTA
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- AAATCTTCCT GTGAATTCCA TTTTAAAGGT AGTCGAGGTG AACCGCGTCT GG - #TCTGCAGA
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- GGATAGAAAA AAGGCCCTCT GATACCTCAA GTTAGTTTCA CCTTTAAAGA AG - #GTCGGAAG
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- TAAAGACGCA AAGCCTTTCC CGGACGTGCG GAAGGGCAAC GTCCTTCCTC AT - #GGCCGGAA
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- ATGGAAC TTT AATTTCCCGT TCCCCCAAC CAGCCCGCCC GAGAGAGTGA CT - #CTCACGAG
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- AGCCGCGAGA GTCAGCTTGG CCAATCCGTG CGGTCGGCGG CCGCTCCCTT TA - #TAAGCCGA
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- CTCGCCCCGGC AGCGCACCGG GTTGCGGAGG GTGGGCCTGG GAGGGGTGGT GG - #CCATTTTTT
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- TGTCTAACCC TAACTGAGAA GGGCGTAGGC GCCGTGCTTT TGCTCCCCGC GC - #GCTGTTTTT
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- TCTCGCTGAC TTTCAGCGGG CGGAAAAGCC TCGGCCTGCC GCCTTCCACC GT - #TCATTCTA
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- GAGCAAACAA AAAATGTCAG CTGCTGGCCC GTTCGCCCCCT CCCGGGGACC TG - #CGGCGGGT
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- CGCCTGCCCA GCGCCCGAAC CCCGCCTGGA GGCCGCGGTC GGCCCGGGGC TT - #CTCCGGAG
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- GCACCCACTG CCACCGCGAA GAGTTGGGCT CTGTCAGCCG CGGGTCTCTC GG - #GGGCGAGG
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- GCGAGGTTCA GGCCTTTTCAG GCCGCAGGAA GAGGAACGGA GCGAGTCCCC GC - #GCGCGGCG
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- CGATTCCCTG AGCTGTGGGA CGTGACCCCA GGACTCGGCT CACACATGCA GT - #TCGCTTTC
1920
- CTGTTGGTGG GGGGAACGCC GATCGTGCGC ATCCGTCAAC CCTCGCCGGC AG - #TGGGGGCT
1980
- TGTGAACCCC CAAACCTGAC TGACTGGGCC AGTGTGCTGC AAATTGGCAG GA - #GACGTGAA
2040
- GGCACCTCCA AAGTCGGCCA AAATGAATGG GCAGTGAGCC GGGGTTGCCT GG - #AGCCGTTT
2100
- CTGCGTGGGT TCTCCCGTCT TCCGCTTTTT GTTGCTTTTT ATGGTTGTAT TA - #CAACTTAG
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- TTCCTGCTCT GCAGATTTTG TTGAGGTTTT TGCTTCTCCC AAGGTAGATC TC - #GACCAGTC
2220
- CCTCAACGGG GTGTGGGGAG AACAGTCATT TTTTTTTGAG AGATCATTTA AC - #ATTTAATG
2280
- AATATTTAAT TAGAAGATCT AAATGAACAT TGGAAATTGT GTTCCTTTAA TG - #GTCATCGG
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- TTTATGCCAG AGGTTAGAAG TTTCTTTTTT GAAAAATTAG ACCTTGCGCA TG - #ACCTTGAG
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#           2426 CCAC AAGCTT
- (2) INFORMATION FOR SEQ ID NO:5:
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              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: RNA
-   (ix) FEATURE:
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          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: RNA
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              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
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#                22NNN NN
-      (2) INFORMATION FOR SEQ ID NO:8:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA (genomic)
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
# 20                AACC
-      (2) INFORMATION FOR SEQ ID NO:9:
-      (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 9 base p - #airs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
#                9
-      (2) INFORMATION FOR SEQ ID NO:10:
-      (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 9 base p - #airs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
#                9
-      (2) INFORMATION FOR SEQ ID NO:11:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 10 base
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
#                10
-      (2) INFORMATION FOR SEQ ID NO:12:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 10 base
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
#                10
-      (2) INFORMATION FOR SEQ ID NO:13:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 39 base
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
# 39                UCCG UGAGGACGAA ACAAAAAAU
-      (2) INFORMATION FOR SEQ ID NO:14:
-      (i) SEQUENCE CHARACTERISTICS:

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#pairs      (A) LENGTH: 37 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

-          (ii) MOLECULE TYPE: RNA
-          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
#           37          CCGU GAGGACGAAA GACAAAA
- (2) INFORMATION FOR SEQ ID NO:15:
-          (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 36 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-          (ii) MOLECULE TYPE: RNA
-          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
#           36          CCGU GAGGACGAAA GGGUUA
- (2) INFORMATION FOR SEQ ID NO:16:
-          (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 36 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-          (ii) MOLECULE TYPE: RNA
-          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
#           36          CCGU GAGGACGAAA CCCGCG
- (2) INFORMATION FOR SEQ ID NO:17:
-          (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-          (ii) MOLECULE TYPE: DNA
-          (ix) FEATURE:
              (A) NAME/KEY: modified.sub.-- - #base
              (B) LOCATION: 20
#/mod.sub.-- base= OTHERRMATION:
#"N = 3'-aminoadenosine"
-          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
#           20          TTCN
- (2) INFORMATION FOR SEQ ID NO:18:
-          (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-          (ii) MOLECULE TYPE: DNA
-          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
#           20          CTAT
- (2) INFORMATION FOR SEQ ID NO:19:
-          (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 12 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-          (ii) MOLECULE TYPE: RNA
-          (ix) FEATURE:
              (A) NAME/KEY: modified.sub.-- - #base
              (B) LOCATION: 1
#/mod.sub.-- base= umNFORMATION:
-          (ix) FEATURE:
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                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 2
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 3
#/mod.sub.-- base= OTHERRMATION:
#"N = 2'-O-methyladenosine"
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 4
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 5
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 6
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 7
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 8
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 9
#/mod.sub.-- base= OTHERRMATION:
#"N = 2'-O-methyladenosine"
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 10
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 11
#/mod.sub.-- base= iINFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 12
#/mod.sub.-- base= OTHERRMATION:
#"N = biotinylated inosine"
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
#          12
-      (2) INFORMATION FOR SEQ ID NO:20:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 12 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 1
#/mod.sub.-- base= OTHERRMATION:
#"N = 2'-O-methyladenosine"
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 2
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:

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                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 3
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 4
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 5
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 6
#/mod.sub.-- base= gmNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 7
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 8
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 9
#/mod.sub.-- base= OTHERRMATION:
#"N = 2'-O-methyladenosine"
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 10
#/mod.sub.-- base= umNFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 11
#/mod.sub.-- base= iINFORMATION:
-      (ix) FEATURE:
                (A) NAME/KEY: modified.sub.-- - #base
                (B) LOCATION: 12
#/mod.sub.-- base= OTHERRMATION:
#"N = biotinylated inosine"
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
#          12
-      (2) INFORMATION FOR SEQ ID NO:21:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 17 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
#          17          G
-      (2) INFORMATION FOR SEQ ID NO:22:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 17 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
#          17          G
-      (2) INFORMATION FOR SEQ ID NO:23:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 30 base
              (B) TYPE: nucleic acid

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                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
#          30      GGGG AGCAAAAGCA
- (2) INFORMATION FOR SEQ ID NO:24:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 26 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
#          26      ACGG TGGAAG
- (2) INFORMATION FOR SEQ ID NO:25:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
# 20          GAGG
- (2) INFORMATION FOR SEQ ID NO:26:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 21 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
#21          CAGC A
- (2) INFORMATION FOR SEQ ID NO:27:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 25 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
#          25      GCTG ACATT
- (2) INFORMATION FOR SEQ ID NO:28:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
# 20          TTCA
- (2) INFORMATION FOR SEQ ID NO:29:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 28 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
#          28      GGGA GCAAAGCA
- (2) INFORMATION FOR SEQ ID NO:30:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 26 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
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-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
#          26  AAGG GCGTAG
- (2) INFORMATION FOR SEQ ID NO:31:
-      (i) SEQUENCE CHARACTERISTICS:
-          (A) LENGTH: 9 base p - #airs
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
#          9
- (2) INFORMATION FOR SEQ ID NO:32:
-      (i) SEQUENCE CHARACTERISTICS:
-          (A) LENGTH: 9 base p - #airs
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: RNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
#          9
- (2) INFORMATION FOR SEQ ID NO:33:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 17 base
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
#      17          A
- (2) INFORMATION FOR SEQ ID NO:34:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 24 base
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
#          24AAAC CCAA
- (2) INFORMATION FOR SEQ ID NO:35:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 18 base
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
#      18          AA
- (2) INFORMATION FOR SEQ ID NO:36:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 18 base
-          (B) TYPE: nucleic acid
-          (C) STRANDEDNESS: single
-          (D) TOPOLOGY: linear
-      (ii) MOLECULE TYPE: DNA
-      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
#      18          CC
- (2) INFORMATION FOR SEQ ID NO:37:
-      (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 22 base
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